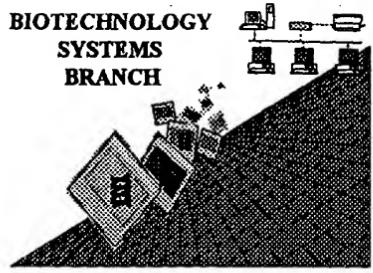


0200

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/507968
Art Unit / Team No. : 0186
Date Processed by STIC: 3/10/2020

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/507,968

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.
AKS-Biotechnology Systems Branch- 5/15/99

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/507,968DATE: 03/10/2000
TIME: 10:14:25

Input Set: I507968.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

1 <110> Yu, Guo-Liang
2 Ebner, Reinhard
3 Ni, Jian
4 Rosen, Craig A.
5 <120> Neutrokine-alpha and Neutrokine-alpha Splice Variants
6 <130> PF343P3
7 <140> US/09/507,968
8 <141> 2000-02-22
9 <150> 60/122,388
10 <151> 1999-03-02
11 <150> 60/124,097
12 <151> 1999-03-12
13 <150> 60/126,599
14 <151> 1999-03-26
15 <150> 60/127,598
16 <151> 1999-04-02
17 <150> 60/130,412
18 <151> 1999-04-16
19 <150> 60/130,696
20 <151> 1999-04-23
21 <150> 60/131,278
22 <151> 1999-04-27
23 <150> 09/255,794
24 <151> 1999-02-23
25 <150> 60/131,673
26 <151> 1999-04-29
27 <150> 60/136,784
28 <151> 1999-05-28
29 <150> 60/142,659
30 <151> 1999-07-06
31 <150> 60/145,824
32 <151> 1999-07-27
33 <150> 60/167,239
34 <151> 1999-11-24
35 <150> 60/168,624
36 <151> 1999-12-03
37 <150> 60/171,108
38 <151> 1999-12-16
39 <150> 60/171,626
40 <151> 1999-12-23
41 <150> 60/176,015
42 <151> 2000-01-14
43 <160> 38
44 <170> PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/507,968

DATE: 03/10/2000
TIME: 10:14:25

Input Set: I507968.RAW

ERRORED SEQUENCES FOLLOW

E--> 45 <210> 1
46 <211> 1100
47 <212> DNA
48 <213> Homo sapiens *next page*
49 <220>
50 <221> CDS
51 <222> (147)..(1001)
52 <400> 1
53 aaattcagga taactctcct gaggggtgag ccaagccctg ccatgtagtg cacgcaggac 60
54 atcaacaaac acagataaca ggaaatgata cattccctgt ggtcacttat tctaaaggcc 120
55 ccaaccttca aagttcaagt agtgat atg gat gac tcc aca gaa agg gag cag 173
56 Met Asp Asp Ser Thr Glu Arg Glu Gln
57 1 5
58 tca cgc ctt act tct tgc ctt aag aaa aga gaa gaa atg aaa ctg aag 221
59 Ser Arg Leu Thr Ser Cys Leu Lys Lys Arg Glu Glu Met Lys Leu Lys
60 10 15 20 25
61 gag tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct gtc cga tcc 269
62 Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser
63 30 35 40
64 tcc aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg gca ctg ctg 317
65 Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu
66 45 50 55
67 tct tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc gcc ctg caa 365
68 Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala Ala Leu Gln
69 60 65 70
70 ggg gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac cac gcg gag 413
71 Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu
72 75 80 85
73 aag ctg cca gca gga gca gga gcc ccc aag gcc ggc ctg gag gaa gct 461
74 Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala
75 90 95 100 105
76 cca gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca gct cca gga 509
77 Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro Ala Pro Gly
78 110 115 120
79 gaa ggc aac tcc agt cag aac agc aga aat aag cgt gcc gtt cag ggt 557
80 Glu Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala Val Gln Gly
81 125 130 135
82 cca gaa gaa aca gtc act caa gac tgc ttg caa ctg att gca gac agt 605
83 Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser
84 140 145 150
85 gaa aca cca act ata caa aaa gga tct tac aca ttt gtt cca tgg ctt 653
86 Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val Pro Trp Leu
87 155 160 165
88 ctc agc ttt aaa agg gga agt gcc cta gaa gaa aaa gag aat aaa ata 701
89 Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu Asn Lys Ile

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/507,968DATE: 03/10/2000
TIME: 10:14:25

Input Set: I507968.RAW

```

90      170      175      180      185
91      ttg gtc aaa gaa act ggt tac ttt ttt ata tat ggt cag gtt tta tat 749
92      Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly Gln Val Leu Tyr
93              190              195              200
94      act gat aag acc tac gcc atg gga cat cta att cag agg aag aag gtc 797
95      Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg Lys Lys Val
96              205              210              215
97      cat gtc ttt ggg gat gaa ttg agt ctg gtg act ttg ttt cga tgt att 845
98      His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile
99              220              225              230
100     caa aat atg cct gaa aca cta ccc aat aat tcc tgc tat tca gct ggc 893
101     Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly
102              235              240              245
103     att gca aaa ctg gaa gaa gga gat gaa ctc caa ctt gca ata cca aga 941
104     Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala Ile Pro Arg
105     250              255              260              265
106     gaa aat gca caa ata tca ctg gat gga gat gtc aca ttt ttt ggt gca 989
107     Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr Phe Phe Gly Ala
108              270              275              280
E--> 109     ttg aaa ctg ctg tgacctactt acaccatgtc tgtagctatt ttcctccctt
110     1041
111     Leu Lys Leu Leu
112              285
E--> 113     tctctgtacc tctaagaaga aagaatctaa ctgaaaatac caaaaaaaaaa aaaaaaaaaa
W--> 114     1100

```

format
error
(see
item 1
on
Error
summary
sheet)

```

115     <210> 22
E--> 116     <211> 1040
117     <212> DNA
118     <213> Homo sapiens
119     <220>
120     <221> CDS
121     <222> (1)..(468)
122     <400> 22
123     cgc gtg gta gac ctc tca gct cct cct gca cca tgc ctg cct gga tgc 48
124     Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys
125     1              5              10              15
126     cgc cat tct caa cat gat gat aat gga atg aac ctc aga aac aga act 96
127     Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
128     20              25              30
129     tac aca ttt gtt cca tgg ctt ctc agc ttt aaa aga gga aat gcc ttg 144
130     Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu
131     35              40              45
132     gag gag aaa gag aac aaa ata gtg gtg agg caa aca ggc tat ttc ttc 192
133     Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
134     50              55              60
135     atc tac agc cag gtt cta tac acg gac ccc atc ttt gct atg ggt cat 240
136     Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
137     65              70              75              80
138     gtc atc cag agg aag aaa gta cac gtc ttt ggg gac gag ctg agc ctg 288

```

see next page

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/507,968

DATE: 03/10/2000
TIME: 10:14:25

Input Set: I507968.RAW

```

139      Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
140              85              90              95
141      gtg acc ctg ttc cga tgt att cag aat atg ccc aaa aca ctg ccc aac   336
142      Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
143              100              105              110
144      aat tcc tgc tac tcg gct ggc atc gcg agg ctg gaa gaa gga gat gag   384
145      Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
146              115              120              125
147      att cag ctt gca att cct cgg gag aat gca cag att tca cgc aac gga   432
148      Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
149              130              135              140
150      gac gac acc ttc ttt ggt gcc cta aaa ctg ctg taa ctcaattgct       478
151      Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
152      145              150              155
153      ggagtgcgtg atcccccttc ctgctcttct ctgtacctcc gagggagaaa cagacgactg 538
154      gaaaaactaa aagatgggga aagccgtcag cgaaagtttt ctctgtaccc gttgaatctg 598
155      atccaaacca ggaaatataa cagacagcca caaccgaagt gtgccatgtg agttatgaga 658
156      aacggagccc gcgctcagaa agaccggatg aggaagaccg ttttctccag tcctttgcca 718
157      acacgcaccg caaccttgct ttttgccttg ggtgacacat gttcagaatg cagggagatt 778
158      tccttgtttt gcgatttgcc atgagaagag ggcccacaac tgcaggtcac tgaagcattc 838
159      acgctaagtc tcaggattta ctctcccttc tcatgctaag tacacacacg ctcttttcca 898
160      ggtaatacta tgggatacta tggaaagggt gtttgttttt aaatctagaa gtcttgaact 958
E--> 161      ggcaatagac aaaaatcctt ataaattcaa gtgtaaaata aacttaatta aaaaggttta 1018
162      1018
E--> 163      agtgtgaaaa aaaaaaaaaa aa
164      1040

```

same error (pointing to line 161)

1040 (pointing to line 163)

```

165      <210> 38
166      <211> 177
167      <212> DNA
168      <213> Mus musculus
169      <400> 38
W--> 170      mdsaktcccc kgdmkvgydt kgawgcrdgr aatassstam syaaadmirr syrgsataaa 60
W--> 171      gatagvktaa rhssrghrn rragtdvdsa acgrhshdd ngmrrdcad sdtakkvvr 120
W--> 172      tgyysvytda mghvrkkvhv gdsvtromk tnnacysaga rgdarbasrn gddtgak 177
E--> 173      25

```

See 10-11 (pointing to line 171)

delete at end of file (pointing to line 173)

Err summary sheet (handwritten note)

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

✓ FYI

Input Set: I507968.RAW

Line	Error/Warning	Original Text
46	E Input 1100, Calc# Bases 989 differ	<211> 1100
109	E Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
113	E Wrong Amino Acid Designator	tctctgtacc tctaagaaga aagaatctaa ctgaaaat
113	E Wrong Amino Acid Designator	tctctgtacc tctaagaaga aagaatctaa ctgaaaat
113	E Wrong Amino Acid Designator	tctctgtacc tctaagaaga aagaatctaa ctgaaaat
113	E Wrong Amino Acid Designator	tctctgtacc tctaagaaga aagaatctaa ctgaaaat
113	E Wrong Amino Acid Designator	tctctgtacc tctaagaaga aagaatctaa ctgaaaat
113	E Wrong Amino Acid Designator	tctctgtacc tctaagaaga aagaatctaa ctgaaaat
114	W Invalid/Missing Amino Acid Numbering	1100
116	E Input 1040, Calc# Bases 958 differ	<211> 1040
161	E Wrong Amino Acid Designator	ggcaatagac aaaaatcctt ataaattcaa gtgtaaaa
161	E Wrong Amino Acid Designator	ggcaatagac aaaaatcctt ataaattcaa gtgtaaaa
161	E Wrong Amino Acid Designator	ggcaatagac aaaaatcctt ataaattcaa gtgtaaaa
161	E Wrong Amino Acid Designator	ggcaatagac aaaaatcctt ataaattcaa gtgtaaaa
161	E Wrong Amino Acid Designator	ggcaatagac aaaaatcctt ataaattcaa gtgtaaaa
161	E Wrong Amino Acid Designator	ggcaatagac aaaaatcctt ataaattcaa gtgtaaaa
163	E Wrong Amino Acid Designator	agtgtgaaaa aaaaaaaaaa aa
163	E Wrong Amino Acid Designator	agtgtgaaaa aaaaaaaaaa aa
163	E Wrong Amino Acid Designator	agtgtgaaaa aaaaaaaaaa aa
170	W "N" or "Xaa" used: Feature required	mdsaktcccs kgdmkvgydt kgawgcrdgr aatassst
171	W "N" or "Xaa" used: Feature required	gatagvktaa rhnssrghrn rragtdvdsa acgcrhsh
172	W "N" or "Xaa" used: Feature required	tgyysvytda mghvrkkvhv gdsvtrcnmk tnnscysa
173	E Number of Bases conflict w/ Running Total	25